

#C/OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/873,637

DATE: 08/07/2001
TIME: 08:24:20

Input Set : A:\Jeffrey.app
Output Set: N:\CRF3\08072001\I873637.raw

3 <110> APPLICANT: Ross, Jeffrey
 5 <120> TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
 6 (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
 8 <130> FILE REFERENCE: 960296.95131
 10 <140> CURRENT APPLICATION NUMBER: US/09/873,637
 11 <141> CURRENT FILING DATE: 2001-06-04
 13 <160> NUMBER OF SEQ ID NOS: 46
 15 <170> SOFTWARE: PatentIn Ver. 2.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2224
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Mus musculus
 22 <400> SEQUENCE: 1
 23 ggggtgggtg sgtagaaaagt ttgcggctcc cgccggccgt atccacgcct atcggcatag 60
 24 gaggatatacc gcccgcgcc cccggatcg gcattgaatg gaacagtgtc ctggccccgc 120
 25 caccggccacc atgaacaagg tttacatcg cAACCTCAAC gagagtgtga ccccccgcaga 180
 26 ctggagaaa gtattcgcgg agcacaagat ctcctacagc ggccagttct tggtcaaatc 240
 27 cggctacgccc ttcgtggatt gccccgacga gcaactggcg atgaaggcca tcgaaacttt 300
 28 ctcggggaaa gtagaactgc aaggaaaacg tctagagatt gaacactcag tccccaaaaaa 360
 29 acaaaggagt cgaaaaatac agatccgcaa tattccaccc cagctccgat gggaaagtgc 420
 30 agatagcctg ctggctcagt acggtaatgt ggagaactgt gagcaagtga acactgaaag 480
 31 tgagacagcg gtggtcaacg tcacctactc taaccgggag cagaccaggc aagctatcat 540
 32 gaagctaaat ggccatcaac tggagaacca tgcctgaag gtctcctaca tacctgatga 600
 33 gcagataaca caaggtcctg agaatggcg tcgtggaggc tttgggtctc gggccagcc 660
 34 ccggcaaggg tcgcccgtgg cagcaggggc tccagccaa cagcagccag tggacatccc 720
 35 tctccggctc ctgggccta cgcgttatgt aggctatc attggcaagg agggtgccac 780
 36 catccgaaac atcacaaaac agacgcagtc caaaatagac gtgcataatggg aggagaatgc 840
 37 gggcgctgcg gagaaggcca tcagcgtgca ttcaacccct gaaggctgt cctccgcgtg 900
 38 caagatgatc ttggagatta tgcacaagg gcaaaggac accaaaacgg cagatgaagt 960
 39 tcccctgaag atcctggctc ataacaactt cgtcggcga ctcattggca aggaaggccg 1020
 40 gaacctgaag aagggtggagc aggacacaga gacgaagatc accatctcat cgctccagga 1080
 41 cctcacgctc tataaccctg agaggaccat cactgtgaag ggcgcattt agaacttttg 1140
 42 caggcccgag caggagatca tgaagaaaagt tcgagaggct tacgagaacg acgtggccgc 1200
 43 catgagcttgc cagtcacc tcacccctgg gcttaacccct gctgctgttag gtctttccc 1260
 44 agtttcatcc agcgctgtcc ctcctcctcc cagcagtgtc actggggctg ctccctatag 1320
 45 ctccttcatg caggctccgg agcaggagat ggtacaagt ttcatccccg cccaggctgt 1380
 46 gggcgccatc attggcaaga agggccagca catcaaaca ctctccctt tcgcccagcgc 1440
 47 ctccatcaag attgctccac cagaaacacc tgactccaa gttcgaatgg tcgtcatcac 1500
 48 tggaccccca gaggtcagt tcaaggctca gggagaatt tatggcaaacc taaaagaaga 1560
 49 gaatttcttt ggtcccaagg aggaagtaaa gctagagacc cacatacggg ttccggcttc 1620
 50 agcagccggc cgcgtcatcg gcaaaggcgg caaaacggg aatgagctgc agaacttgac 1680
 51 tgcagctgag gtggtagtgc caagagacca gacccggat gagaacgacc aagtcattgt 1740
 52 taagatcatc ggacatttct atgccagcca gatggctcag cggaaagatcc gagacatcct 1800
 53 ggctcaagtt aagcaacagc accagaaggg acagagcaac ctggcccagg cacggaggaa 1860
 54 gtgaccccgcc cccctcctgt cccattggct ccaagatcag caggaggaac acagaactgg 1920
 55 agggggcggtt ggagggccgg tgtttttc ccagcaggcc tgagaatgag tggaaatcag 1980
 56 ggcatttggg cctggctgga gatcagggtt gcacactgta ttgagaacaa tggccagtg 2040

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57 aggaatcctg atctctcgcc cccaatttag ccagctggcc acagcccacc ccttggata 2100
58 tcaccattgc aatcatagct tggtttgctt ttaaacgtgg attgtcttga agttctccag 2160
59 cctccatgga aggtatgggtc agatcccagt gggaaagaga aataaaaattt ctttcagggt 2220
60 ttat 2224
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 577
64 <212> TYPE: PRT
65 <213> ORGANISM: Mus musculus
67 <400> SEQUENCE: 2
68 Met Asn Lys Leu Tyr Ile Gly Asn Leu Asn Glu Ser Val Thr Pro Ala
69 1 5 10 15
71 Asp Leu Glu Lys Val Phe Ala Glu His Lys Ile Ser Tyr Ser Gly Gln
72 20 25 30
74 Phe Leu Val Lys Ser Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu His
75 35 40 45
77 Trp Ala Met Lys Ala Ile Glu Thr Phe Ser Gly Lys Val Glu Leu Gln
78 50 55 60
80 Gly Lys Arg Leu Glu Met Glu His Ser Val Pro Lys Lys Gln Arg Ser
81 65 70 75 80
83 Arg Lys Ile Gln Ile Arg Asn Ile Pro Pro Gln Leu Arg Trp Glu Val
84 85 90 95
86 Leu Asp Ser Leu Leu Ala Gln Tyr Gly Thr Val Glu Asn Cys Glu Gln
87 100 105 110
89 Val Asn Thr Glu Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Asn
90 115 120 125
92 Arg Glu Gln Thr Arg Gln Ala Ile Met Lys Leu Asn Gly His Gln Leu
93 130 135 140
95 Glu Asn His Ala Leu Lys Val Ser Tyr Ile Pro Asp Glu Gln Ile Thr
96 145 150 155 160
98 Gln Gly Pro Glu Asn Gly Arg Arg Gly Gly Phe Gly Ser Arg Gly Gln
99 165 170 175
101 Pro Arg Gln Gly Ser Pro Val Ala Ala Gly Ala Pro Ala Lys Gln Gln
102 180 185 190
104 Pro Val Asp Ile Pro Leu Arg Leu Leu Val Pro Thr Gln Tyr Val Gly
105 195 200 205
107 Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
108 210 215 220
110 Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
111 225 230 235 240
113 Glu Lys Ala Ile Ser Val His Ser Thr Pro Glu Gly Cys Ser Ser Ala
114 245 250 255
116 Cys Lys Met Ile Leu Glu Ile Met His Lys Glu Ala Lys Asp Thr Lys
117 260 265 270
119 Thr Ala Asp Glu Val Pro Leu Lys Ile Leu Ala His Asn Asn Phe Val
120 275 280 285
122 Gly Arg Leu Ile Gly Lys Glu Gly Arg Asn Leu Lys Lys Val Glu Gln
123 290 295 300
125 Asp Thr Glu Thr Lys Ile Thr Ile Ser Ser Leu Gln Asp Leu Thr Leu
126 305 310 315 320

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128 Tyr Asn Pro Glu Arg Thr Ile Thr Val Lys Gly Ala Ile Glu Asn Cys
129           325           330           335
131 Cys Arg Ala Glu Gln Glu Ile Met Lys Lys Val Arg Glu Ala Tyr Glu
132           340           345           350
134 Asn Asp Val Ala Ala Met Ser Leu Gln Ser His Leu Ile Pro Gly Leu
135           355           360           365
137 Asn Leu Ala Ala Val Gly Leu Phe Pro Ala Ser Ser Ser Ala Val Pro
138           370           375           380
140 Pro Pro Pro Ser Ser Val Thr Gly Ala Ala Pro Tyr Ser Ser Phe Met
141 385           390           395           400
143 Gln Ala Pro Glu Gln Glu Met Val Gln Val Phe Ile Pro Ala Gln Ala
144           405           410           415
146 Val Gly Ala Ile Ile Gly Lys Lys Gly Gln His Ile Lys Gln Leu Ser
147           420           425           430
149 Arg Phe Ala Ser Ala Ser Ile Lys Ile Ala Pro Pro Glu Thr Pro Asp
150           435           440           445
152 Ser Lys Val Arg Met Val Val Ile Thr Gly Pro Pro Glu Ala Gln Phe
153           450           455           460
155 Lys Ala Gln Gly Arg Ile Tyr Gly Lys Leu Lys Glu Glu Asn Phe Phe
156 465           470           475           480
158 Gly Pro Lys Glu Glu Val Lys Leu Glu Thr His Ile Arg Val Pro Ala
159           485           490           495
161 Ser Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu
162           500           505           510
164 Leu Gln Asn Leu Thr Ala Ala Glu Val Val Val Pro Arg Asp Gln Thr
165           515           520           525
167 Pro Asp Glu Asn Asp Gln Val Ile Val Lys Ile Ile Gly His Phe Tyr
168           530           535           540
170 Ala Ser Gln Met Ala Gln Arg Lys Ile Arg Asp Ile Leu Ala Gln Val
171 545           550           555           560
173 Lys Gln Gln His Gln Lys Gly Gln Ser Asn Leu Ala Gln Ala Arg Arg
174           565           570           575
176 Lys
180 <210> SEQ ID NO: 3
181 <211> LENGTH: 14
182 <212> TYPE: PRT
183 <213> ORGANISM: Mus musculus
185 <400> SEQUENCE: 3
186 Arg Arg Gly Gly Phe Gly Ser Arg Gly Gln Pro Arg Gln Gly
187   1           5           10
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 14
192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 4
196 Gly Arg Arg Gly Leu Gly Gln Arg Gly Ser Ser Arg Gln Gly
197   1           5           10
200 <210> SEQ ID NO: 5
201 <211> LENGTH: 14

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202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 5
206 Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly
207 1 5 10
210 <210> SEQ ID NO: 6
211 <211> LENGTH: 13
212 <212> TYPE: PRT
213 <213> ORGANISM: Homo sapiens
215 <400> SEQUENCE: 6
216 Gly Arg Gly Gly Phe Gly Asp Arg Gly Gly Arg Gly Gly
217 1 5 10
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 14
222 <212> TYPE: PRT
223 <213> ORGANISM: Homo sapiens
225 <400> SEQUENCE: 7
226 Gly Arg Gly Gly Phe Gly Gly Arg Gly Gly Arg Gly Gly
227 1 5 10
230 <210> SEQ ID NO: 8
231 <211> LENGTH: 14
232 <212> TYPE: PRT
233 <213> ORGANISM: Homo sapiens
235 <400> SEQUENCE: 8
236 Leu Arg Arg Gly Asp Gly Arg Arg Gly Gly Gly Arg Gly
237 1 5 10
240 <210> SEQ ID NO: 9
241 <211> LENGTH: 13
242 <212> TYPE: PRT
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Consensus sequence for SEQ ID NOS:3-8.
248 <400> SEQUENCE: 9
249 Gly Arg Gly Gly Phe Gly Arg Gly Gly Arg Gly Gly
250 1 5 10
253 <210> SEQ ID NO: 10
254 <211> LENGTH: 11
255 <212> TYPE: PRT
256 <213> ORGANISM: Mus musculus
258 <400> SEQUENCE: 10
259 Gln Leu Arg Trp Glu Val Leu Asp Ser Leu Leu
260 1 5 10
263 <210> SEQ ID NO: 11
264 <211> LENGTH: 11
265 <212> TYPE: PRT
266 <213> ORGANISM: Homo sapiens
268 <400> SEQUENCE: 11
269 His Leu Gln Trp Glu Val Leu Asp Ser Leu Leu
270 1 5 10

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273 <210> SEQ ID NO: 12
274 <211> LENGTH: 10
275 <212> TYPE: PRT
276 <213> ORGANISM: Homo sapiens
278 <400> SEQUENCE: 12
279 Gln Leu Arg Leu Glu Arg Leu Gln Ile Asp
280 1 5 10
283 <210> SEQ ID NO: 13
284 <211> LENGTH: 11
285 <212> TYPE: PRT
286 <213> ORGANISM: Homo sapiens
288 <400> SEQUENCE: 13
289 Thr Ile Ser Ser Leu Gln Asp Leu Thr Leu Tyr
290 1 5 10
293 <210> SEQ ID NO: 14
294 <211> LENGTH: 11
295 <212> TYPE: PRT
296 <213> ORGANISM: Homo sapiens
298 <400> SEQUENCE: 14
299 Thr Ile Ser Pro Leu Gln Glu Leu Thr Leu Tyr
300 1 5 10
303 <210> SEQ ID NO: 15
304 <211> LENGTH: 11
305 <212> TYPE: PRT
306 <213> ORGANISM: Human immunodeficiency virus
308 <400> SEQUENCE: 15
309 Gln Leu Pro Pro Leu Glu Arg Leu Thr Leu Asp
310 1 5 10
313 <210> SEQ ID NO: 16
314 <211> LENGTH: 7
315 <212> TYPE: PRT
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Consensus sequence for SEQ ID NOS:10-15.
321 <400> SEQUENCE: 16
322 Gln Leu Leu Glu Leu Thr Leu
323 1 5
326 <210> SEQ ID NO: 17
327 <211> LENGTH: 47
328 <212> TYPE: PRT
329 <213> ORGANISM: Mus musculus
331 <400> SEQUENCE: 17
332 Leu Leu Val Pro Thr Gln Tyr Val Gly Ala Ile Ile Gly Lys Glu Gly
333 1 5 10 15
335 Ala Thr Ile Arg Asn Ile Thr Lys Gln Thr Gln Ser Lys Ile Asp Val
336 20 25 30
338 His Arg Lys Glu Asn Ala Gly Ala Ala Glu Lys Ala Ile Ser Val
339 35 40 45
342 <210> SEQ ID NO: 18

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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\Jeffrey.app
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L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45